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AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application.

1. (Currently Amended) A method comprising:

predicting a secondary structure of a protein;

annealing the predicted secondary structure;

superimposing the annealed [[predicted]] secondary structure on a set of topomers;

refining the superimposed secondary structure; and

predicting a tertiary structure of [[a]] the protein based on the refined secondary structure.
2. (Currently Amended) The method of claim 1, wherein said [[predicted]] predicting the secondary structure comprises deriving [[is]] a consensus predicted secondary structure.
3. (Currently Amended) The method of claim 1, [[further comprising]] wherein annealing [[the secondary structure by]] comprises annealing by energy minimization.
4. (Original) The method of claim 3, wherein said energy minimization is by a random Monte Carlo method.
5. (Original) The method of claim 4, wherein the random Monte Carlo method uses random moves from a log probability table.

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6. (Currently Amended) The method of claim ~~[[3]]~~ 4, wherein the random Monte Carlo method ~~[[uses smart moves]]~~ randomly chooses an amino acid to move.
7. (Currently Amended) The method of claim 1, wherein refining the superimposed secondary structure ~~[[the secondary structure superimposed on a set of topomers is refined by]]~~ comprises refining by energy minimization.
8. (Currently Amended) The method of claim 7, wherein refining the superimposed secondary structure ~~[[the secondary structure superimposed on a set of topomers is refined using]]~~ comprises refining using a molecular modeling program.
9. (Currently Amended) The method of claim 8, whercin the molecular modeling program ~~[[is]]~~ comprises X-PLOR.
10. (Currently Amended) The method of claim 1, wherein ~~[[the protein]]~~ predicting the secondary structure ~~[[is predicted]]~~ comprises predicting the secondary structure by at least one technique selected from the group consisting of Chou-Fasmand and GOR (Garnier, Osguthorbe and Robson).
11. (Currently Amended) The method of claim 1, wherein ~~[[the protein]]~~ predicting the secondary structure ~~[[is predicted]]~~ comprises predicting the secondary structure by at least one program selected from the group consisting of PSI-pred, JPRED, Prof, PREDATOR, PHD, ZPRED, mPredict, BMERC, PSA Server, SSP and PROFsec.
12. (Currently Amended) The method of claim 1, ~~[[wherein]]~~ further comprising deriving the set of topomers ~~[[is derived]]~~ using Continuous Configuration Boltzman Biased Direct Monte Carlo Method.
13. (Currently Amended) The method of claim 1, wherein refining the superimposed secondary structure ~~[[is refined]]~~ comprises refining the superimposed secondary
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structure by a program selected from the group consisting of AMBER, CHARMM, X-PLOR and INSIGHTII.

14. (New) The method of claim 1, wherein said annealing the predicted secondary structure comprises choosing a secondary structure prediction from a plurality of secondary structure predictions for an amino acid based at least in part on respective probabilities.

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